

SEQUENCE LISTING

<110> Yu Lin
Lin Sun
Long V. Nguyen
Howard M. Goodman

<120> MODIFICATION OF PLANT STORAGE RESERVES

<130> 00786/368002

<150> 60/128,651
<151> 1999-04-08

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1483
<212> DNA
<213> Arabidopsis thaliana

<400> 1

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aatggaa	gt	tataagcaat	gggttggag	aaatagagag	tatgtacaat	180
c	tttgccaa	ac	ggattgacat	ggctgcttcc	tgagaagtt	240
agaagcagta	acggctttt	tggcata	cacaacgata	aatgaacaca	taattgaaaa	300
tgctccaaca	cctcg	tgcc	atgttggatc	ttccggaa	at	360
actactcatc	gccatc	c	aggatttgg	aactgttgc	gatccatccc	420
ctatggagac	aaaaaaatg	g	actacattat	tctca	tttcttatcc	480
gttagcctt	g	ttccg	gata	gtgcttctt	caaggaggg	540
tgaggagaaa	gattctaacc	aatccgagtc	gc	aaataga	aaacaccta	600
tctcg	ggc	c	atgttgc	tttgc	taatt	660
ggcgtgtct	catgtt	ctt	gaaaccaaaa	tcatcataat	cggttagaaaa	720
gcttaagtt	catt	gg	tttgc	ccatg	act tggaaggacg	780
cgg	tttgc	tca	aatgcaaga	acta	tttccatcccc	840
gttgg	tttac	taac	gagacc	tttca	ctgtgtttgc	900
tgagg	tttac	taa	gttggat	tc	tcagaaaata	960
tcttcttgc	tttgc	tttgc	tttgc	tttgc	tttgc	1020
tgaaaaggat	tttgc	tttgc	tttgc	tttgc	tttgc	1080
attcttcacc	tttgc	tttgc	tttgc	tttgc	tttgc	1140
tccattgatc	tttgc	tttgc	tttgc	tttgc	tttgc	1200
gtacacttac	tttgc	tttgc	tttgc	tttgc	tttgc	1260
atatcggtt	tttgc	tttgc	tttgc	tttgc	tttgc	1320
aggaaatgg	tttgc	tttgc	tttgc	tttgc	tttgc	1380
ccatagacag	tttgc	tttgc	tttgc	tttgc	tttgc	1440
atgtatctga	tttgc	tttgc	tttgc	tttgc	tttgc	1483
gaataaaaca	tttgc	tttgc	tttgc	tttgc	tttgc	
agcatcatta	tttgc	tttgc	tttgc	tttgc	tttgc	
aagattaaaa	tttgc	tttgc	tttgc	tttgc	tttgc	
aaaaaaa	tttgc	tttgc	tttgc	tttgc	tttgc	
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<210> 2
<211> 367
<212> PRT
<213> Arabidopsis thaliana

<400> 2
Met Glu Ala Tyr Lys Gln Trp Val Trp Arg Asn Arg Glu Tyr Val Gln
1 5 10 15
Ser Phe Gly Ser Phe Ala Asn Gly Leu Thr Trp Leu Leu Pro Glu Lys
20 25 30
Phe Ser Ala Ser Glu Ile Gly Pro Glu Ala Val Thr Ala Phe Leu Gly
35 40 45
Ile Phe Thr Thr Ile Asn Glu His Ile Ile Glu Asn Ala Pro Thr Pro
50 55 60
Arg Gly His Val Gly Ser Ser Gly Asn Asp Pro Ser Leu Ser Tyr Pro
65 70 75 80
Leu Leu Ile Ala Ile Leu Lys Asp Leu Glu Thr Val Val Glu Val Ala
85 90 95
Ala Glu His Phe Tyr Gly Asp Lys Lys Trp Asn Tyr Ile Ile Leu Thr
100 105 110
Glu Ala Met Lys Ala Val Ile Arg Leu Ala Leu Phe Arg Asn Ser Gly
115 120 125
Tyr Lys Met Leu Leu Gln Gly Gly Glu Thr Pro Asn Glu Glu Lys Asp
130 135 140
Ser Asn Gln Ser Glu Ser Gln Asn Arg Ala Gly Asn Ser Gly Arg Asn
145 150 155 160
Leu Gly Pro His Gly Leu Gly Asn Gln Asn His His Asn Pro Trp Asn
165 170 175
Leu Glu Gly Arg Ala Met Ser Ala Leu Ser Ser Phe Gly Gln Asn Ala
180 185 190
Arg Thr Thr Ser Ser Thr Pro Gly Trp Ser Arg Arg Ile Gln His
195 200 205
Gln Gln Ala Val Ile Glu Pro Pro Met Ile Lys Glu Arg Arg Arg Thr
210 215 220
Met Ser Glu Leu Leu Thr Glu Lys Gly Val Asn Gly Ala Leu Phe Ala
225 230 235 240
Ile Gly Glu Val Leu Tyr Ile Thr Arg Pro Leu Ile Tyr Val Leu Phe
245 250 255
Ile Arg Lys Tyr Gly Val Arg Ser Trp Ile Pro Trp Ala Ile Ser Leu
260 265 270
Ser Val Asp Thr Leu Gly Met Gly Leu Leu Ala Asn Ser Lys Trp Trp
275 280 285
Gly Glu Lys Ser Lys Gln Val His Phe Ser Gly Pro Glu Lys Asp Glu
290 295 300
Leu Arg Arg Arg Lys Leu Ile Trp Ala Leu Tyr Leu Met Arg Asp Pro
305 310 315 320
Phe Phe Thr Lys Tyr Thr Arg Gln Lys Leu Glu Ser Ser Gln Lys Lys
325 330 335
Leu Glu Leu Ile Pro Leu Ile Gly Phe Leu Thr Glu Lys Ile Val Glu
340 345 350
Leu Leu Glu Gly Ala Gln Ser Arg Tyr Thr Tyr Ile Ser Gly Ser

355

360

365

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 3
atcagagatt gatttaacgt a

21

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
acgattttca attatgtgtt c

21

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
cgcttggtcg gtcatttcg

19

<210> 6
<211> 391
<212> PRT
<213> Yarrowia lipolytica

<400> 6
Met Thr Asp Lys Leu Val Lys Val Met Gln Lys Lys Ser Ala Pro
1 5 10 15
Gln Thr Trp Leu Asp Ser Tyr Asp Lys Phe Leu Val Arg Asn Ala Ala
20 25 30
Ser Ile Gly Ser Ile Glu Ser Thr Leu Arg Thr Val Ser Tyr Val Leu
35 40 45
Pro Gly Arg Phe Asn Asp Val Glu Ile Ala Thr Glu Thr Leu Tyr Ala
50 55 60
Val Leu Asn Val Leu Gly Leu Tyr His Asp Thr Ile Ile Ala Arg Ala
65 70 75 80

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Val Ala Ala Ser Pro Asn Ala Ala Val Tyr Arg Pro Ser Pro His
85 90 95
Asn Arg Tyr Thr Asp Trp Phe Ile Lys Asn Arg Lys Gly Tyr Lys Tyr
100 105 110
Ala Ser Arg Ala Val Thr Phe Val Lys Phe Gly Glu Leu Val Ala Glu
115 120 125
Met Val Ala Lys Lys Asn Gly Gly Glu Met Ala Arg Trp Lys Cys Ile
130 135 140
Ile Gly Ile Glu Gly Ile Lys Ala Gly Leu Arg Ile Tyr Met Leu Gly
145 150 155 160
Ser Thr Leu Tyr Gln Pro Leu Cys Thr Thr Pro Tyr Pro Asp Arg Glu
165 170 175
Val Thr Gly Glu Leu Leu Glu Thr Ile Cys Arg Asp Glu Gly Glu Leu
180 185 190
Asp Ile Glu Lys Gly Leu Met Asp Pro Gln Trp Lys Met Pro Arg Thr
195 200 205
Gly Arg Thr Ile Pro Glu Ile Ala Pro Thr Asn Val Glu Gly Tyr Leu
210 215 220
Leu Thr Lys Val Leu Arg Ser Glu Asp Val Asp Arg Pro Tyr Asn Leu
225 230 235 240
Leu Ser Arg Leu Asp Asn Trp Gly Val Val Ala Glu Leu Leu Ser Ile
245 250 255
Leu Arg Pro Leu Ile Tyr Ala Cys Leu Leu Phe Arg Gln His Val Asn
260 265 270
Lys Thr Val Pro Ala Ser Thr Lys Ser Lys Phe Pro Phe Leu Asn Ser
275 280 285
Pro Trp Ala Pro Trp Ile Ile Gly Leu Val Ile Glu Ala Leu Ser Arg
290 295 300
Lys Met Met Gly Ser Trp Leu Leu Arg Gln Arg Gln Ser Gly Lys Thr
305 310 315 320
Pro Thr Ala Leu Asp Gln Met Glu Val Lys Gly Arg Thr Asn Leu Leu
325 330 335
Gly Trp Trp Leu Phe Arg Gly Glu Phe Tyr Gln Ala Tyr Thr Arg Pro
340 345 350
Leu Leu Tyr Ser Ile Val Ala Arg Leu Glu Lys Ile Pro Gly Leu Gly
355 360 365
Leu Phe Gly Ala Leu Ile Ser Asp Tyr Leu Tyr Leu Phe Asp Arg Tyr
370 375 380
Tyr Phe Thr Ala Ser Thr Leu
385 390

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
ggcaatattc ttccgttgc

<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
aaaaatqqaa ctacattatt ctc

23

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<210> 9  
<211> 22  
<212> DNA  
<213> Artificial Sequence
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<220>
<223> Primer

<221> variation
<222> (1)...(22)
<223> Where h is a, c, or t/u; not g.

<400> 9
ataagtaaaa cgcttaacct hc

22